Output tables for 1xN statistical comparisons.

December 17, 2022

1 Average rankings of Friedman Alligned test

Average ranks obtained by each method in the Friedman Alligned test.

Algorithm	Ranking
MEABC	140.1034
ABCADE	95.1034
ABCNG	117.4483
SHADE	95.7241
MAPSO	128.6552
TAPSO	72.6552
MEEABC	64.3103

Table 1: Average Rankings of the algorithms (Aligned Friedman)

Aligned Friedman statistic (distributed according to chi-square with 6 degrees of freedom): 24.106446.
P-value computed by Aligned Friedman Test: 0.000499227654.

2 Post hoc comparison (Friedman Alligned)

P-values obtained in by applying post hoc methods over the results of Friedman Alligned procedure.

i	algorithm	$z = (R_0 - R_i)/SE$	p	Holm	Hochberg	Hommel	Holland	Rom
6	MEABC	4.912937	0.000001	0.008333	0.008333	0.008333	0.008512	0.008764
5	MAPSO	4.170856	0.00003	0.01	0.01	0.01	0.010206	0.010515
4	ABCNG	3.44442	0.000572	0.0125	0.0125	0.0125	0.012741	0.013109
3	SHADE	2.036254	0.041725	0.016667	0.016667	0.016667	0.016952	0.016667
2	ABCADE	1.99602	0.045932	0.025	0.025	0.025	0.025321	0.025
1	TAPSO	0.540915	0.588566	0.05	0.05	0.05	0.05	0.05

Table 2: Post Hoc comparison Table for $\alpha = 0.05$ (FRIEDMAN ALLIGNED)

Bonferroni-Dunn's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.008333.
Holm's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016667.
Hochberg's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.0125.
Hommel's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016667.
Holland's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016952.
Rom's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.013109.

3 Adjusted P-Values (Friedman Alligned)

Adjusted P-values obtained through the application of the post hoc methods (Friedman Alligned).

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	$p_{Hochberg}$	p_{Hommel}
1	MEABC	0.000001	0.000005	0.000005	0.000005	0.000005
2	MAPSO	0.00003	0.000182	0.000152	0.000152	0.000152
3	ABCNG	0.000572	0.003434	0.002289	0.002289	0.002289
4	SHADE	0.041725	0.250349	0.125175	0.091863	0.08345
5	ABCADE	0.045932	0.27559	0.125175	0.091863	0.091863
6	TAPSO	0.588566	3.531398	0.588566	0.588566	0.588566

Table 3: Adjusted p-values (ALIGNED FRIEDMAN) (I)

i	algorithm	unadjusted p	$p_{Holland}$	p_{Rom}
1	MEABC	0.000001	0.000005	0.000005
2	MAPSO	0.00003	0.000152	0.000144
3	ABCNG	0.000572	0.002287	0.002183
4	SHADE	0.041725	0.120024	0.091863
5	ABCADE	0.045932	0.120024	0.091863
6	TAPSO	0.588566	0.588566	0.588566

Table 4: Adjusted p-values (ALIGNED FRIEDMAN) (II)